II. AMENDMENT

A. In the Specification:

Upon review of the amendment submitted on December 19, 2005 it has been observed that two conflicting instructions were included on page 5 and similarly on page 6. In particular, on page 5, two instructions were requested to "*... amend the paragraph at page 18, lines 8-16 as follows.*" It is respectfully submitted that the second instruction should have read as follows.

Please amend the paragraph at page 19, lines 10-26 as follows:

For example, the proteolytic enzyme trypsin is a serine protease that cleaves peptide bonds between lysine or arginine and an unspecific amino acid to thereby produce peptides that comprise an amine terminus (N-terminus) and lysine or arginine carboxyl terminal amino acid (C-terminus). In this way the peptides from the cleavage of the protein are predictable and their presence and/or quantity, in a sample from a trypsin digest, can be indicative of the presence and/or quantity of the protein of their origin. Moreover, the free amine termini of a peptide can be a good nucleophile that facilitates its labeling. Other exemplary proteolytic enzymes include papain, pepsin, ArgC, LysC, V8 protease, AspN, pronase, chymotrypsin and carboxypeptid[e]ase C.

For example, a protein (e.g. protein Z‴) might produce three peptides (e.g. peptides B, C and D) when digested with a protease such as trypsin. Accordingly, a sample that has been digested with a proteolytic enzyme, such as trypsin, and that when analyzed is confirmed to contain peptides B, C and D, can be said to have originally comprised the protein Z‴. The quantity of peptides B, C and D will also correlate with the quantity of protein Z‴ in the sample that was digested. In this way, any determination of the identity and/or quantify of one or more of peptides B, C and D in a sample (or a fraction thereof), can be used to identify and/or quantify protein Z‴ in the original sample (or a fraction thereof).

Similarly, on page 6, two instructions were requested to "*... amend the paragraph at page 21, line 25 to page 22, line 6 as follows:* It is respectfully submitted that the second instruction should have read as follows.

Please amend the paragraph at page 24, lines 22-31 as follows:

For example, the analyte might be a peptide that resulted from the degradation of a protein using an enzymatic digestion reaction to process the sample. Protein degradation can be accomplished by treatment of the sample with a proteolytic enzyme (e.g. trypsin, papain, pepsin, ArgC, LysC, V8 protease, AspN, pronase, chymotrypsin or carboxypeptid[e]ase C). By determination of the identity and amount of a peptide in a sample mixture and identifying the sample from which it originated, optionally coupled with the determination of other peptides from that sample ~~sample~~, the precursor protein to the degraded peptide can be identified and/or quantified with respect to the sample from which it originated. Because this method allows for the multiplex determination of a protein, or proteins, in more than one sample (i.e. from a sample mixture), it is a multiplex method.

Accordingly, it is requested that the specification be amended as indicated and that the faulty instructions at pages 5 and 6 of the response dated December 19, 2006 be disregarded.